#2



OIPE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,156

DATE: 03/19/2002 P.5

TIME: 16:22:30

Input Set : A:\EP.txt

```
3 <110> APPLICANT: Bristol-Myers Squibb Company
      5 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNITS,
              K+betaM4 and K+betaM5
      8 <130> FILE REFERENCE: D0115NP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/086,156
C--> 10 <141> CURRENT FILING DATE: 2002-02-28
     10 <150> PRIOR APPLICATION NUMBER: US 60/272,190
     11 <151> PRIOR FILING DATE: 2001-02-28
     13 <150> PRIOR APPLICATION NUMBER: US 60/274,258
     14 <151> PRIOR FILING DATE: 2001-03-07
     16 <160> NUMBER OF SEQ ID NOS: 98
     18 <170> SOFTWARE: PatentIn version 3.0
     20 <210> SEQ ID NO: 1
     21 <211> LENGTH: 1839
     22 <212> TYPE: DNA
     23 <213> ORGANISM: homo sapiens
     25 <220> FEATURE:
     26 <221> NAME/KEY: CDS
     27 <222> LOCATION: (5)..(1057)
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                                                                                49
     31
             Met Thr Gly Ser His Asp Val Ile Gly Gly Ala Gly Lys Gln Val
     34 ctc tgc tgc ttt tgc aag cag aga aat aag agt ttg ggc acc tac cca
                                                                                97
     35 Leu Cys Cys Phe Cys Lys Gln Arg Asn Lys Ser Leu Gly Thr Tyr Pro
                                             25
                        20
     38 ggg gtc cca ggg aat gcc ctg tgg ctc ctg acc tcc ccc gcc tgt aat
                                                                               145
     39 Gly Val Pro Gly Asn Ala Leu Trp Leu Leu Thr Ser Pro Ala Cys Asn
                    35
                                         40
     42 gct ctg agc act tca gca gta atg cat gga aga gat aag ggg tct gtg
                                                                               193
     43 Ala Leu Ser Thr Ser Ala Val Met His Gly Arg Asp Lys Gly Ser Val
     46 acc cat gga act gtc caa gtc ctc tct gac acc cgc ttc ttt tcc tgc
                                                                               241
     47 Thr His Gly Thr Val Gln Val Leu Ser Asp Thr Arg Phe Phe Ser Cys
                                70
     50 cqt qaa qqa cta ctt cca qca acc cag tct cct qcc atg tcc qac ccc
                                                                               289
     51 Arg Glu Gly Leu Leu Pro Ala Thr Gln Ser Pro Ala Met Ser Asp Pro
                                                 90
                            85
     54 atc acg ctg aac gtc ggg ggg aag ctc tat aca acc tca ctg gcg acc
                                                                               337
     55 Ile Thr Leu Asn Val Gly Gly Lys Leu Tyr Thr Thr Ser Leu Ala Thr
                                             105
                        100
     <u>58_ctg_acc_agc_ttc_cct_gac_tcc_atg_cta_ggc_gcc_atg_ttc_agc_ggg_aag----</u> ---
     59 Leu Thr Ser Phe Pro Asp Ser Met Leu Gly Ala Met Phe Ser Gly Lys
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Input Set : A:\EP.txt

62 atg ccc acc aag agg gac agc cag ggc aac tgc ttc att gac cgt gac 63 Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp 64 130 135 140 140 135 140 140 145 145 150 150 155 155 150 155 155 150 155 155	60 115 120 125	
63 Met Pro Thr Lys Arg Asp Ser Gln Gly Asn Cys Phe Ile Asp Arg Asp 64 130 130 140 140 140 140 150 155 140 140 140 150 155 150 166 ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt 481 67 Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu 158 145 150 155 170 155 170 155 170 175 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 170 175 175 170 175 170 175 175 170 175 175 170 175 175 170 175 175 170 175 175 170 175 170 175 175 175 175 175 175 175 175 175 175		433
64 130 135 140 66 ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt 67 Gly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu 68 145 150 155 70 gac ctg cct gag gac ttc cag gag atg ggc ctg ctc cgc agg gag gcc 71 Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala 72 160 165 170 175 74 gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag agg gac 75 Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu 76 180 195 200 78 gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg 79 Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu 80 195 200 82 aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gca ccc cag 83 Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln 84 210 215 220 86 atc tac agc ctc tcc tct tcc agc atg agg ggc ttc aac atc acc tg 79 11e Tyr Ser Leu Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile 82 25 230 235 90 ttc agc acc tcc tgc ctc ttc ctc aag ctc ctt ggc tta aag ctc ttc 91 Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe 92 240 245 250 255 94 tac tgc tcc aat ggc aat ctc tcc tc ac ac agc aca ttg cag gag 95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp 96 260 265 270 98 ccc ac ac ac ctg act ctg agc ag ac ctg gtg gca ag ggc ctg ca 96 pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro 100 275 280 285 102 gag gag gag tac acc aca gaa acc tcc ag ag gtc ttc gca gag gag tcd ctg ca 103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 104 290 295 300 105 300 106 gcc ac aca gag atc acc aca gcd tcc ag gtc ttc gca gag gag tcd ctg ca 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315 110 aaa atc gct ctg agc gat gct tc tgc at gat gtt ttc cac cac act 1009 11 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335 114 gct ctg gat ttt aga aca at aat att att cga tta ata cgg tcc agc cac acc acc cacacacacacac tggagatggg gagtccacac aggccatgt gagccagtccac		
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67 cly Lys Val Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser His Leu 68 145 150 155 155 70 gac ctg cct gag gac ttc cag gag atg ggg ctg ctc cgc agg gag gcc 529 71 Asp Leu Pro Glu Asp Phe Gln Glu Met Gly Leu Leu Arg Arg Glu Ala 72 160 165 170 73 gac ttc tac cag gtg cag ccc ctg att gag gcc ctg cag gag aag gaa 577 75 Asp Phe Tyr Gln Val Gln Pro Leu Ile Glu Ala Leu Gln Glu Lys Glu 76 180 185 190 78 gtg gag ctc tcc aag gcc gag aag aat gcc atg ctc aac atc aca ctg 79 Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu 80 195 200 205 82 aac cag cgt gtg cag acg gtc cac ttc act gtg cgc gag gac ccc cag 83 Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln 84 210 215 220 86 atc tac agc ctc tct tct cag atg gag gtc ttc aac gcc aac atc 87 Ile Tyr Ser Leu Ser Ser Ser Met Glu Val Phe Asn Ala Asn Ile 88 225 230 235 90 ttc agc acc tcc tgc ctc ttc tct aag ctc ttg gct gag ctc tac gcc aac atc 91 Phe Ser Thr Ser Cys Leu Phe Leu Lys Leu Leu Gly Ser Lys Leu Phe 92 240 245 250 250 94 tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac 95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ser Ile Thr Ser His Leu Gln Asp 96 260 260 265 97 Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro 100 275 102 gag gag gag gat cac acc aag cac ctc aag acc ctc tgg gtg gcc aat gtg gag gcc ct gcc 103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 104 290 295 105 gc aac aac aag cat cac aag ctc caag gcc ttc gg gtg gcc aat gtg gag gg gtg gtg gcc 106 gcc aac aac aag cat cac aag ctc tcg agc gtg gcc aat gtg gag gag gag ctg 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 109 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cac at 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro 110 110 aaa atc gct ctg gat gac aat aaa att atc tcga tta ata cgg tac agg 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350	66 ggc aaa gtg ttc cgc tat atc ctc aac ttc ctg cgg acc tcc cac ctt	481
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79 Val Glu Leu Ser Lys Ala Glu Lys Asn Ala Met Leu Asn Ile Thr Leu 80	· -	
80		625
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83 Asn Gln Arg Val Gln Thr Val His Phe Thr Val Arg Glu Ala Pro Gln 84		
84		673
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92 240 245 250 255  94 tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac 817  95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp 260 265 270  98 ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca 865  99 Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro 275 280 285  102 gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc 913  103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 290 295 300  106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg 961  107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009  111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 12 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057  115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccagtc 1117		769
94 tac tgc tcc aat ggc aat ctc tcc tcc atc acc agc cac ttg cag gac 95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp 96		
95 Tyr Cys Ser Asn Gly Asn Leu Ser Ser Ile Thr Ser His Leu Gln Asp 96	22 23	017
96		817
98 ccc aac cac ctg act ctg gac tgg gtg gcc aat gtg gag ggc ctg cca 99 Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro 100 275 280 285  102 gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc 913 103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 104 290 295 300  106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg 961 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335 114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350 118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
99 Pro Asn His Leu Thr Leu Asp Trp Val Ala Asn Val Glu Gly Leu Pro 100	200	0.65
100       275       280       285         102       gag gag gag tac acc acc acc acc acc acc acc acc acc		865
102 gag gag gag tac acc aag cag aac ctc aag agg ctc tgg gtg gtg ccc 103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 104 290 295 300  106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
103 Glu Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro 104 290 295 300  106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg 961 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117	· · · · · · · · · · · · · · · · · · ·	013
104       290       295       300         106       gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg       961         107       Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu       305       310       315         110       aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat       1009         111       Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His       335         112       320       325       330       335         114       gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg       1057         115       Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg       340       345       350         118       taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc       1117		313
106 gcc aac aag cag atc aac agc ttc cag gtc ttc gtg gaa gag gta ctg 107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315 110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335 114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350 118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
107 Ala Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu 108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009  111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057  115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117	<del></del>	961
108 305 310 315  110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009  111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His  112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057  115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg  116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		701
110 aaa atc gct ctg agc gat ggc ttc tgc atc gat tct tct cac cca cat 1009 111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335 114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350 118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
111 Lys Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His 112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057  115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		1009
112 320 325 330 335  114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057  115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg  116 340 345 350  118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		1005
114 gct ctg gat ttt atg aac aat aag att att cga tta ata cgg tac agg 1057 115 Ala Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg 116 340 345 350 118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
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116 340 345 350 118 taaaaggacc ccaacaacac tggagatggg gagtcccagg aagctcatgt cagccaggtc 1117		
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		1117
120 Lluyadudca Lclcdccadl ddldcdaddc addddal actaatccat attaattgcg 1177	120 ttggagggca tctcgccagt ggtgcgaggc aggggactat actaatctgt attaattgtg	1177
122 tagcaggact tgattccccc catgatgaag tccacctttt ggaatccagt gtcctctgaa 1237		
124 cagaaccacc ttttttcttg ccattttgag ctgcagacag gcggtttatt atgacaagtg 1297		
126 aagagtcagc tgatgtgtac taaaggaggc cataggagga ttttccagcc aggacaaaag 1357		1357
128 agcagcagtt ttctcctggg ctccatctct ctgtaccgct agccagtgcc gcatttatcc 1417		1417

Input Set : A:\EP.txt

132 134 136 138 140 142 144 147 148 149	ccas ccas ttcs gags tcas tags aa <210 <211	ggacated to aggardate agggardate	ata a cgt d agc d gag d att d	aagtoggatoggatoggatoggaatgo	cccca gttt ttag cagge gctt aaat : 2	ag co gc co tg to ca ga ta ga ca c	ggtte cagge cccci agtte aaage ttcca	ectg ggtga tette eagaa ggte aaat	t cae a cca g ggg a ggg t gcf	cacci atgti ggtca tagga tatci	tgct ttgg agag aatg tttg	cctocctocctocctocctocct	cccto gctto aggto ctcto aaato	gga agtg g tga t	caggo atgct gcago taggo caag	agttaa gtgcat tgtgca ggtcta gctgaa tatctg aaaaaa	1477 1537 1597 1657 1717 1777 1837 1839
152	2 <400> SEQUENCE: 2																
154	Met	Thr	Gly	Ser	His	Asp	Val	Ile	Gly	Gly	Ala	Gly	Lys	Gln	Val	Leu	
155			-		5	-			_	10		-	-		15		
		Cys	Phe	Cys	Lys	Gln	Arq	Asn	Lys	Ser	Leu	Gly	Thr	Tyr	Pro	Gly	
159	-1-	- 1		20	1				25			- 4		30		_	
	Va 1	Pro	Gly		Ala	Leu	Trp	Len	Leu	Thr	Ser	Pro	Ala	Cvs	Asn	Ala	
163			35					40					45	0,2			
	T.011	Ser	Thr	Ser	Δla	Val	Met		Glv	Arσ	Asn	Lvs		Ser	Va 1	Thr	
167	пси	50	1111	001	2124	,	55	*****	0-1	**** 9		60	0-1	501	,		
	Hic		Thr	Va 1	Gln	Val		Ser	Δsn	Thr	Δrα		Dhe	Ser	Cvs	Δrσ	
171		Ory	1111	Vu_	OIII	70	LCu	DCI	SP	1111	75	1110	1110	UCI	Cys	80	
		Clv	Leu	Lau	Dro		Thr	Gln	Sor	Dro		Mat	Sor	Aen	Dro		
175	GIU	СТУ	пеп	пеп	85	лта	1111	GTII	per	90	AIG	Mec	Ser	изр	95	116	
	mb~	Tou	Asn	Wa 1		C117	Tvc	T OU	Пттт		mh r	Cor	LOU	λla		Lou	
179	1111	ьeu	ASII	100	GIY	СТУ	пуз	ьец	105	1111	1111	Set	neu	110	1111	neu	
	шhх	Con	Phe		7 an	C07	Mot	T OU		7 l a	Mot	Dho	Cor		Two	Mot	
183	1111	ser	115	PIU	ASP	Set	Met	120	GIY	ніа	Met	File	125	GTÄ	цуз	Mec	
	Dro	mh∞	Lys	7 22	λαη	Cor	Cln	-	λan	Cvc	Dho	T10		λ τα	Nan	C1 v	
187	PIO	130	ьуѕ	AIG	ASP	ser	135	GTA	ASII	Cys	Pile	140	ASP	мту	ASP	GIY	
	Tvc		Phe	λνα	Щттъ	Tlo		λan	Dho	T OII	λκα	-	Sor	Uic	LOU	λcn	
	145	vai	FIIC	лгу	TYT	150	Leu	usii	FILE	пец	155	1111	Ser	птэ	цец	160	
		Dro	Glu	7 cn	Dho		Clu	Mot	Cl <sub>v</sub>	T Ou		λνα	λκα	Clu	λ1 =		
195	пец	FIO	GIU	тэр	165	GIII	GIU	nec	СТУ	170	пец	arg	пту	GIU	175	лэр	
	Dho	Птт	Gln	17 a 1	-	Dro	LOU	Tla	Clu	-	LOU	Cln	Clu	Tvc		Val	
199	rne	TÄT	GTII	180	GIII	PIO	цец	TIE	185	ніа	Leu	GIII	Gru	190	GIU	Val	
	Clu	Tou	Ser		λla	Clu	Lvc	λan	-	Mot	LOU	λαη	T10		LOU	λen	
202	GIU	ьeu	195	ьуѕ	на	GIU	гЛЯ	200	нта	Met	ьea	ASII	205	1111	ьeu	ASII	
	Cln	7 ~~	Val	Cln	Thr	17 - 1	uic		Пhr	Wa I	7 × ~	C1.1		Dro	Cln	т10	
207	GIII	210	Val	GIII	1111	val	215	Pile	1111	Val	Arg	220	ніа	PIO	GIII	iie	
	Птт х		Lou	Cor	Cor	Cor		Mot	C111	17 a 1	Dho		λla	Nan	т1 о	Dho	
	225	Set	Leu	Set	PET	230	SET	MEC	GIU	val	235	นอแ	та	HOII	116	240	
		ሞኮァ	Ser	Cvc	Lou		Lou	Tare	Lou	Lou		Ser	Lare	Leu	Dhe		
214	Set	TIIT	Ser	Cys	245	FIIE	пец	пуъ	ьец	250	GTA	SET	nys	neu	255	- A -	
	Cve	Sor	Asn	<u> </u>		Lou	Sor	Ser	т16		Sor	uic	Leu	Gln		Dro	
219	Cys	Ser	LOII	260	LOII	neu.	DET	JGI	265	T 11T	SET	птэ	பசம	270	ռոհ	210	
	Δen	uie	Leu		Leu	λen	Фrn	Va 1		λen	Va 1	Glu	G1 v		Dro	Glu	
223	បទព	1113	275	T 11T	шeц	rah	115	280	AIG	បទព	Val	GIU	285	Leu	110	JIU	
			-, 5					250					-55				

Input Set : A:\EP.txt

```
226 Glu Glu Tyr Thr Lys Gln Asn Leu Lys Arg Leu Trp Val Val Pro Ala
                          295
230 Asn Lys Gln Ile Asn Ser Phe Gln Val Phe Val Glu Glu Val Leu Lys
          310
                                   315
234 Ile Ala Leu Ser Asp Gly Phe Cys Ile Asp Ser Ser His Pro His Ala
                  325
                                     330
238 Leu Asp Phe Met Asn Asn Lys Ile Ile Arg Leu Ile Arg Tyr Arg
                                  345 350
239
               340
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 237
244 <212> TYPE: PRT
245 <213> ORGANISM: homo sapiens
247 <400> SEQUENCE: 3
249 Met Asp Asn Gly Asp Trp Gly Tyr Met Met Thr Asp Pro Val Thr Leu
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252 Asn Val Gly Gly His Leu Tyr Thr Thr Ser Leu Thr Thr Leu Thr Arg
                                  2.5
255 Tyr Pro Asp Ser Met Leu Gly Ala Met Phe Gly Gly Asp Phe Pro Thr
258 Ala Arg Asp Pro Gln Gly Asn Tyr Phe Ile Asp Arg Asp Gly Pro Leu
261 Phe Arg Tyr Val Leu Asn Phe Leu Arg Thr Ser Glu Leu Thr Leu Pro
                      70
264 Leu Asp Phe Lys Glu Phe Asp Leu Leu Arg Lys Glu Ala Asp Phe Tyr
                   85
267 Gln Ile Glu Pro Leu Ile Gln Cys Leu Asn Asp Pro Lys Pro Leu Tyr
              100
                                 105
270 Pro Met Asp Thr Phe Glu Glu Val Val Glu Leu Ser Ser Thr Arg Lys
          115
                              120
273 Leu Ser Lys Tyr Ser Asn Pro Val Ala Val Ile Ile Thr Gln Leu Thr
                          135
276 Ile Thr Thr Lys Val His Ser Leu Leu Glu Gly Ile Ser Asn Tyr Phe
                       150
                                          155
279 Thr Lys Trp Asn Lys His Met Met Asp Thr Arg Asp Cys Gln Val Ser
        165
                                     170
282 Phe Thr Phe Gly Pro Cys Asp Tyr His Gln Glu Val Ser Leu Arg Val
    180
                                 185
285 His Leu Met Glu Tyr Ile Thr Lys Gln Gly Phe Thr Ile Arg Asn Thr
    195
                              200
288 Arg Val His His Met Ser Glu Arg Ala Asn Glu Asn Thr Val Glu His
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291 Asn Trp Thr Phe Cys Arg Leu Ala Arg Lys Thr Asp Asp
292 225
                       230
294 <210> SEQ ID NO: 4
295 <211> LENGTH: 256
296 <212> TYPE: PRT
297 <213> ORGANISM: homo sapiens
299 <220> FEATURE:
300, <221> NAME/KEY: UNSURE
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Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J086156.raw

```
301 <222> LOCATION: (15)..(15)
     302 <223> OTHER INFORMATION: wherein "X" is equal to any amino acid.
     305 <400> SEQUENCE: 4
W--> 307 Met Ser Arg Pro Leu Ile Thr Arg Ser Pro Ala Ser Pro Leu Xaa Asn
     310 Gln Gly Ile Pro Thr Pro Ala Gln Leu Thr Lys Ser Asn Ala Pro Val
     313 His Ile Asp Val Gly Gly His Met Tyr Thr Ser Ser Leu Ala Thr Leu
     316 Thr Lys Tyr Pro Glu Ser Arg Ile Gly Arg Leu Phe Asp Gly Thr Glu
     319 Pro Ile Val Leu Asp Ser Leu Lys Gln His Tyr Phe Ile Asp Arg Asp
                             70
     322 Gly Gln Met Phe Arg Tyr Ile Leu Asn Phe Leu Arg Thr Ser Lys Leu
                                             90
                         85
     325 Leu Ile Pro Asp Asp Phe Lys Asp Tyr Thr Leu Leu Tyr Glu Glu Ala
                                         105
     328 Lys Tyr Phe Gln Leu Gln Pro Met Leu Leu Glu Met Glu Arg Trp Lys
                                     120
     331 Gln Asp Arg Glu Thr Gly Arg Phe Ser Arg Pro Cys Glu Cys Leu Val
             130
                                 135
     334 Val Arq Val Ala Pro Asp Leu Gly Glu Arg Ile Thr Leu Ser Gly Asp
                             150
     337 Lys Ser Leu Ile Glu Glu Val Phe Pro Glu Ile Gly Asp Val Met Cys
                         165
                                             170
     340 Asn Ser Val Asn Ala Gly Trp Asn His Asp Ser Thr His Val Ile Arg
                     180
                                         185
     343 Phe Pro Leu Asn Gly Tyr Cys His Leu Asn Ser Val Gln Val Leu Glu
                                     200
     346 Arg Leu Gln Gln Arg Gly Phe Glu Ile Val Gly Ser Cys Gly Gly Gly
                                 215
     349 Val Asp Ser Ser Gln Phe Ser Glu Tyr Val Leu Arg Arg Glu Leu Arg
                                                 235
                             230
     352 Arg Thr Pro Arg Val Pro Ser Val Ile Arg Ile Lys Gln Glu Pro Leu
    355 <210> SEQ ID NO: 5
    356 <211> LENGTH: 234
     357 <212> TYPE: PRT
    358 <213> ORGANISM: homo sapiens
    360 <400> SEQUENCE: 5
    362 Met Pro His Arg Lys Glu Arg Pro Ser Gly Ser Ser Leu His Thr His
    365 Gly Ser Thr Gly Thr Ala Glu Gly Gly Asn Met Ser Arg Leu Ser Leu
    368 Thr Arg Ser Pro Val Ser Pro Leu Ala Ala Gln Gly Ile Pro Leu Pro
                                     40
    371 Ala Gln Leu Thr Lys Ser Asn Ala Pro Val His Ile Asp Val Gly Ser
    374 His Met Tyr Thr Ser Ser Leu Ala Thr Leu Thr Lys Tyr Pro Asp Ser
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 03/19/2002

PATENT APPLICATION: US/10/086,156

TIME: 16:22:31

Input Set : A:\EP.txt

Output Set: N:\CRF3\03192002\J086156.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 L:525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8